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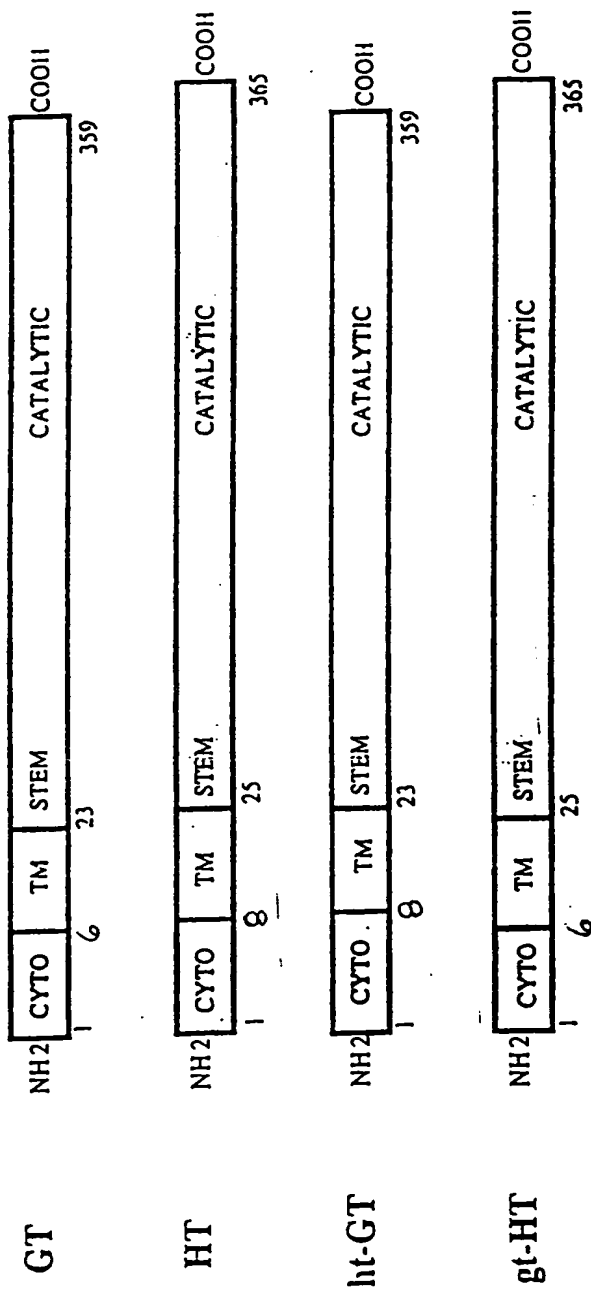


FIGURE 1  
SUBSTITUTE SHEET (Rule 26)

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## PORCINE SECRETOR SEQUENCE

(SEQ ID No. 1)

M L S M Q A S F F P T G P F I L 17  
 CT ACA GCC ATG CTC AGC ATG CAG GCA TCC TTC TTC CCC AGG GGT CCC TTC ATC CTC 59  
 F V F T A S T I F H L Q Q R M V K I Q P 37  
 TTT GTC TTC ACG GCT TCC ACC ATA TTT CAC CTT CAG CAG AGG ATG GTG AAG ATT CAA CCC 119  
 T W E L Q M V T Q V T T E S P S P Q L 57  
 ACG TGG GAG TTA CAG ATG GTG ACG CAG GTG ACC-ACA GAG AGC CCC TCG AGC CCC CAG CTG 179

## PORCINE SECRETOR SEQUENCE

K G M W T I N A I G R L G N Q M G E Y A 77  
 AAG GGC ATG TGG ACG ATC AAT GCC ATC GGC CGC CTG GGG AAC CAG ATG GGG GAG TAC GCC 239  
 T L Y A L A R M N G R P A F I P P E M H 97  
 ACC CTG TAC GCG CTG GCC AGG ATG AAC GGG CGG CGG TTC ATC CCG CCC GAG ATG CAC 299  
 S T L A P I F R I T L P V L H A S T A R 117  
 AGC ACG CTG GCC CCC ATC TTC AGG ATC ACC CTC CCG GTC CTG CAC GCC AGC ACG GCC CGC 359  
 R I P W Q N Y H L N D W M E E R Y R H I 137  
 AGG ATC CCC TGG CAG AAC TAC CAC CTG AAC GAC TGG ATG GAG CAG CGG TAC CGC CAC ATC 419  
 P G E Y V R L T G Y P C S W T F Y H H L 157

FIGURE 6

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PIG H TRANSFERASE (SEQ ID No.2)

M W V P S R R H L C L T F L - L U C V L A	20
ATGTGGGTCCCCAGCCGCGCCACCTCTCTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA	60
L T F F L N W Y Q D L F Y S G L D L L A	40
GCAATTTTCTCTCTGAACGCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC	120
L C P D R H N V V S S P V A I F C L A G C	60
CTGTGTCCAGACCATAACSTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCAGC	180
P V H P N A S D S C P K H P A S F S G T	80
CCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC	240
W T I Y P D E R F G N Q H G Q Y A T L L	100
TGGACTATTTACCCGGATGGCCGGTTTGGGAACACAGATGGGACAGTATGCCACGCTGCTG	300
A L A Q L N G R Q A F I Q P A M H A V L	120
GCCCTGGCGCAGCTCAACGGCGCCAGGCGCTTCATCCAGCCTGCCATGCACGCCCTCCTG	360
A P V F P I T L P V L A P E V D R H A P	140
GGCCCGGTGTTCCGCATCAGGCTGCTGTCTCTGGCGCCCGAGGTAGACAGGCACGCTCCT	420
W R E L E L H D W M S E D Y A H L K E P	160
TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC	480
W L K L T G F P C S W T F F H H L R E Q	180
TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG	540
I R S E F T L H D H L R Q E A Q G V L S	200
ATCCGCAGCGAGTTACCCCTGCACGACACCTTCGGCAAGAGGGCCCAGGGGGTACTGAGT	600
Q F R L P R T G D R P S T F V G V H V R	220
CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC	660
R G D Y L R V M P K R W K G V V G D G A	240
CGCGGGGACTATCTCGCTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT	720
Y L Q Q A M D W F R A R Y E A P V F V Y	260
TACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCCGATACGAAGCCCCCGTCTTTGTGGTC	780
T S N G M E W C R K N I D T S R G D V I	280
ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC	840
F A G D G R E A A P A R D F A L L V Q C	300
TTTGCTGGCGATCGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAGTGC	900
N H T I M T I G T F G F W A A Y L A G G	320
AACCACACCATCATGACCATTTGGCACCTTCGGCTTCTGGGCGCGCTACCTGGCTGGTGGA	960
D T I Y L A N F T L P T S S F L K I F K	340
GATACCATCTACTTGGCTAACTTCACCTGCGGACTTCCAGCTTCTGGAAGATCTTTAA	1020
P E A A F L P E W V G I N A D L S P L Q	360
CCCGAGGCTGCCTTCTTCCCGAGTGGGTGGGCATTAAATGCAGACTTGTCTCCACTCCAG	1080
M L A G P	365
ATGTTGGCTGGGCTTGA	1093

FIGURE 7